

1600 #4

2604

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/943,780

DATE: 01/07/2002

TIME: 16:29:39

Input Set : N:\Crf3\RULE60\09943780.raw

Output Set: N:\CRF3\01072602\I943780.raw

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JAN 24 2002
Technology Center 2600RECEIVED
JAN 25 2002
TECH CENTER 1600/2900

ENTERED

RECEIVED
JAN 22 2002
JC 2880 MAIL ROOM

1 <110> APPLICANT: Baker, Kevin
 2 Botstein, David
 3 Eaton, Dan
 4 Ferrara, Napoleone
 5 Filvaroff, Ellen
 6 Gerritsen, Mary
 7 Goddard, Audrey
 8 Godowski, Paul
 9 Grimaldi, Christopher
 10 Gurney, Austin
 11 Hillan, Kenneth
 12 Kljavin, Ivar
 13 Napier, Mary
 14 Roy, Margaret
 15 Tumas, Daniel
 16 Wood, William
 17 <120> TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
 18 ACIDS ENCODING THE SAME
 19 <130> FILE REFERENCE: P2548P1C1
 20 <140> CURRENT APPLICATION NUMBER: 09/943,780
 21 <141> CURRENT FILING DATE: 2001-08-30
 22 <150> PRIOR APPLICATION NUMBER: 09/866,028
 23 <151> PRIOR FILING DATE: 2001-05-25
 27 <160> NUMBER OF SEQ ID NOS: 120
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 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo Sapien
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 35 caccaggact gtgttgaagg gtgtttttt tcttttaaat gtaataacctc 100
 36 cteatctttt cttcttacac agtgtctgag aacatttaca ttatagataa 150
 37 gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
 38 cagtcctaga ctggtcttct acactaagac accatgaagg agtatgtgct 250
 39 cctattattc ctggctttgt gctctgcaa acccttctt agcccttcac 300
 40 acatgcact gaagaatat atgctgaagg atatggaaga cacagatgat 350
 41 gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
 42 tccaacaaga gagccaagaa gccattttt tccatttgat ctgtttccaa 450
 43 tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
 44 ttaggtttga cctcagtcac aaccaacatt ccatttgata ctogaatgct 550
 45 tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gatttttaaag 600
 46 gactcacttc actttatggt ctgacctga acaacaacaa gctaacgaag 650
 47 attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
 48 gtccacaat caactaagt aaataccact taatcttccc aaatcattag 750
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 50 ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaacctct 850
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55  acaacaaaaat cacagatata gaaaatggga gtcttgctaa cataccacgt 1100
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66  cgtacaaaatg atcttacata aatctcatgc ttgaccattc ctttcttcat 1650
67  aacaaaaaag taagatatcc ggtatttaac actttgttat caagcacatt 1700
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70  agagtgcatt acactattct tattctttag taacttgggt agtactgtaa 1850
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81  gctctatata aatgctcaga gttctttatg tattttcttat tggcattcaa 2400
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93      20              25              30
94  Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
95      35              40              45
96  Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
97      50              55              60
98  Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
99      65              70              75
100 Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
101      80              85              90

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104   Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
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106   Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
107                               125                               130           135
108   Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
109                               140                               145           150
110   Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
111                               155                               160           165
112   Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
113                               170                               175           180
114   Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
115                               185                               190           195
116   Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
117                               200                               205           210
118   Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His Ile Arg
119                               215                               220           225
120   Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro
121                               230                               235           240
122   Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val
123                               245                               250           255
124   Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly
125                               260                               265           270
126   Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser Leu Ala
127                               275                               280           285
128   Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu
129                               290                               295           300
130   Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile
131                               305                               310           315
132   Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp
133                               320                               325           330
134   Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala
135                               335                               340           345
136   Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro
137                               350                               355           360
138   Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln Leu Gly
139                               365                               370           375
140   Asn Phe Gly Met
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144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
148 <400> SEQUENCE: 3
149   ggaaatgagt gcaaaccctc 20
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 24

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153 <212> TYPE: DNA
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155 <220> FEATURE:
156 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
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163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
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172 <213> ORGANISM: Homo Sapien
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246 <212> TYPE: PRT

247 <213> ORGANISM: Homo Sapien

248 <400> SEQUENCE: 7

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253 Pro Pro Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val

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